-continued

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1.-38. (canceled)

39. A method for detecting mutations from exposure to a substance, the method comprising:

(a) preparing a sequencing library from a sample comprising a plurality of double-stranded DNA molecules from a patient exposed to the substance, wherein preparing the sequencing library comprises ligating cypher polynucleotides to the double-stranded DNA molecules to form double-stranded cypher-target nucleic acid complexes, wherein the cypher polynucleotides comprise identifier tags selected from a plurality of distinct identifier tag sequences;

(b) sequencing first and second strands of the cypher-target nucleic acid complexes to produce a plurality of first-strand sequencing reads and a plurality of second-strand sequencing reads;

(c) for each cypher-target nucleic acid complex among a plurality of the cypher-target nucleic acid complexes, comparing the first-strand sequencing reads with the second-strand sequencing reads to identify nucleotides in the first strand that have a corresponding complementary nucleotide in the second strand;

(d) detecting a mutation from exposure to the substance by analyzing an error-corrected sequence generated from the first strand sequencing reads and second strand sequencing reads for each of the cypher-target nucleic acid complexes among a plurality of the cypher-target nucleic acid complexes; and comparing the error-corrected sequences to a reference sequence to identify one or more of a mutation, a genomic distribution of mutations, a mutation frequency, sequence heterogeneity, or DNA damage.

40. The method of claim 39, wherein the sample is derived from a human.

41. The method of claim 39, wherein prior to preparing the sequencing library, the method further comprises exposing the patient to the substance.

42. The method of claim 41, wherein prior to exposing the patient to the substance, the patient comprises a normal tissue.

43. The method of claim 39, wherein the sample comprises a blood sample.

44. The method of claim 39, wherein the identifier tag sequences comprise random or partially random sequences.